

SEQUENCE LISTING

<110> PhageTech Inc.

<120> INHIBITORS OF STAPHYLOCOCCUS AUREUS PRIMARY SIGMA FACTOR AND USES THEREOF

<130> SAU-R12-US37-US55

<150> US 60/445,441

<151> 2003-02-07

<160> 41

<170> PatentIn version 3.2

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<212> DNA

<213> Staphylococcus aureus

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tta aca tta gaa gat gtt aag aag caa tta att gaa aaa ggt aaa aaa	96
Leu Thr Leu Glu Asp Val Lys Lys Gln Leu Ile Glu Lys Gly Lys Lys	
20 25 30	
gag ggt cat tta agt cat gaa gaa att gct gaa aaa ctt cag aat ttt	144
Glu Gly His Leu Ser His Glu Glu Ile Ala Glu Lys Leu Gln Asn Phe	
35 40 45	
gat atc gac tct gat caa atg gat gat ttc ttt gat caa tta aat gat	192
Asp Ile Asp Ser Asp Gln Met Asp Asp Phe Phe Asp Gln Leu Asn Asp	
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aat gat att tca cta gtt aat gaa aaa gat agt tca gat act gac gag	240
Asn Asp Ile Ser Leu Val Asn Glu Lys Asp Ser Ser Asp Thr Asp Glu	
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Lys	Leu	Asn	Pro	Ser	Asp	Leu	Ser	Ala	Pro	Pro	Gly	Val	Lys	Ile	Asn	
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gac	cca	gtt	cgt	atg	tac	ctt	aaa	gaa	att	ggg	cgt	gtt	aac	tta	tta	336
Asp	Pro	Val	Arg	Met	Tyr	Leu	Lys	Glu	Ile	Gly	Arg	Val	Asn	Leu	Leu	
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agt	gca	caa	gaa	gaa	atc	gaa	tta	gcc	aaa	cgt	att	gaa	caa	ggt	gat	384
Ser	Ala	Gln	Glu	Glu	Ile	Glu	Leu	Ala	Lys	Arg	Ile	Glu	Gln	Gly	Asp	
		115					120					125				
gaa	gta	gca	aaa	tca	aga	ctt	gca	gaa	gcg	aac	tta	cgt	tta	gtt	gta	432
Glu	Val	Ala	Lys	Ser	Arg	Leu	Ala	Glu	Ala	Asn	Leu	Arg	Leu	Val	Val	
	130					135					140					
agt	att	gct	aaa	aga	tac	gta	ggt	cgt	ggt	atg	tta	ttc	ctt	gat	tta	480
Ser	Ile	Ala	Lys	Arg	Tyr	Val	Gly	Arg	Gly	Met	Leu	Phe	Leu	Asp	Leu	
145					150					155					160	
atc	caa	gaa	ggt	aat	atg	ggt	ctt	att	aaa	gct	gtt	gaa	aaa	ttt	gac	528
Ile	Gln	Glu	Gly	Asn	Met	Gly	Leu	Ile	Lys	Ala	Val	Glu	Lys	Phe	Asp	
				165					170					175		
ttt	aac	aaa	gga	ttt	aag	ttt	tca	aca	tat	gca	aca	tgg	tgg	att	aga	576
Phe	Asn	Lys	Gly	Phe	Lys	Phe	Ser	Thr	Tyr	Ala	Thr	Trp	Trp	Ile	Arg	
		180					185						190			
caa	gca	atc	act	cgt	gca	att	gct	gac	caa	gca	cgt	acg	att	cgt	atc	624
Gln	Ala	Ile	Thr	Arg	Ala	Ile	Ala	Asp	Gln	Ala	Arg	Thr	Ile	Arg	Ile	
		195					200					205				
cct	gtg	cat	atg	gta	gaa	aca	att	aat	aaa	tta	att	cgt	gtt	caa	cgt	672
Pro	Val	His	Met	Val	Glu	Thr	Ile	Asn	Lys	Leu	Ile	Arg	Val	Gln	Arg	
	210					215					220					
caa	tta	tta	cag	gac	tta	ggt	cga	gat	cca	gca	cca	gaa	gaa	att	ggt	720
Gln	Leu	Leu	Gln	Asp	Leu	Gly	Arg	Asp	Pro	Ala	Pro	Glu	Glu	Ile	Gly	
225					230					235					240	
gaa	gaa	atg	gat	tta	cca	gca	gaa	aaa	gtt	cgt	gaa	att	tta	aaa	att	768
Glu	Glu	Met	Asp	Leu	Pro	Ala	Glu	Lys	Val	Arg	Glu	Ile	Leu	Lys	Ile	
				245					250					255		
gcg	caa	gaa	cct	gtt	tca	tta	gaa	aca	cca	att	ggt	gaa	gaa	gat	gat	816

Ala	Gln	Glu	Pro	Val	Ser	Leu	Glu	Thr	Pro	Ile	Gly	Glu	Glu	Asp	Asp		
			260					265					270				
agt	cat	tta	gga	gac	ttt	att	gag	gat	cag	gaa	gca	caa	agt	cct	tca		864
Ser	His	Leu	Gly	Asp	Phe	Ile	Glu	Asp	Gln	Glu	Ala	Gln	Ser	Pro	Ser		
		275					280					285					
gat	cat	gct	gct	tat	gaa	tta	tta	aaa	gag	caa	tta	gaa	gat	gtg	ctt		912
Asp	His	Ala	Ala	Tyr	Glu	Leu	Leu	Lys	Glu	Gln	Leu	Glu	Asp	Val	Leu		
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gat	aca	tta	act	gat	aga	gaa	gaa	aat	gta	tta	cga	tta	aga	ttt	ggc		960
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ctt	gat	gac	ggc	aga	aca	aga	aca	ctt	gaa	gaa	gtt	ggc	aaa	gtt	ttc		1008
Leu	Asp	Asp	Gly	Arg	Thr	Arg	Thr	Leu	Glu	Glu	Val	Gly	Lys	Val	Phe		
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ggc	gtt	aca	cgt	gaa	cgt	att	cga	caa	att	gaa	gca	aaa	gca	ctt	aga		1056
Gly	Val	Thr	Arg	Glu	Arg	Ile	Arg	Gln	Ile	Glu	Ala	Lys	Ala	Leu	Arg		
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aaa	tta	aga	cat	cca	agt	cgt	agt	aaa	cgt	ttg	aaa	gac	ttt	atg	gat		1104
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 <213> Staphylococcus aureus

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		20						25					30		

Glu	Gly	His	Leu	Ser	His	Glu	Glu	Ile	Ala	Glu	Lys	Leu	Gln	Asn	Phe
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35

40

45

Asp Ile Asp Ser Asp Gln Met Asp Asp Phe Phe Asp Gln Leu Asn Asp
 50 55 60

Asn Asp Ile Ser Leu Val Asn Glu Lys Asp Ser Ser Asp Thr Asp Glu
 65 70 75 80

Lys Leu Asn Pro Ser Asp Leu Ser Ala Pro Pro Gly Val Lys Ile Asn
 85 90 95

Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Arg Val Asn Leu Leu
 100 105 110

Ser Ala Gln Glu Glu Ile Glu Leu Ala Lys Arg Ile Glu Gln Gly Asp
 115 120 125

Glu Val Ala Lys Ser Arg Leu Ala Glu Ala Asn Leu Arg Leu Val Val
 130 135 140

Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Met Leu Phe Leu Asp Leu
 145 150 155 160

Ile Gln Glu Gly Asn Met Gly Leu Ile Lys Ala Val Glu Lys Phe Asp
 165 170 175

Phe Asn Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg
 180 185 190

Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile Arg Ile
 195 200 205

Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg Val Gln Arg
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Gln Leu Leu Gln Asp Leu Gly Arg Asp Pro Ala Pro Glu Glu Ile Gly
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Glu Glu Met Asp Leu Pro Ala Glu Lys Val Arg Glu Ile Leu Lys Ile
 245 250 255

Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu Glu Asp Asp
 260 265 270

Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Gln Ser Pro Ser
 275 280 285

Asp His Ala Ala Tyr Glu Leu Leu Lys Glu Gln Leu Glu Asp Val Leu
 290 295 300

Asp Thr Leu Thr Asp Arg Glu Glu Asn Val Leu Arg Leu Arg Phe Gly
 305 310 315 320

Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly Lys Val Phe
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 35 40 45

Phe Asp Phe Asn Lys Gly Phe Lys Phe Ser Thr Tyr Ala Thr Trp Trp
 50 55 60

Ile Arg Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr Ile
 65 70 75 80

Arg Ile Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg Val
 85 90 95

Gln Arg Gln Leu Leu Gln Asp Leu Gly Arg Asp Pro Ala Pro Glu Glu
 100 105 110

Ile Gly Glu Glu Met Asp Leu Pro Ala Glu Lys Val Arg Glu Ile Leu
 115 120 125

Lys Ile Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu Glu
 130 135 140

Asp Asp Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Gln Ser
 145 150 155 160

Pro Ser Asp His Ala Ala Tyr Glu Leu Leu Lys Glu Gln Leu Glu Asp
 165 170 175

Val Leu Asp Thr Leu Thr Asp Arg Glu Glu Asn Val Leu Arg Leu Arg
 180 185 190

Phe Gly Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly Lys
195 200 205

Val Phe Gly Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ala Lys Ala
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Met Asp

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Thr Arg Thr Leu Glu Glu Val Gly Lys Val Phe Gly Val Thr Arg Glu
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Arg Ile Arg Gln Ile Glu Ala Lys Ala Leu Arg Lys Leu Arg His Pro
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Ser Arg Ser Lys Arg Leu Lys Asp Phe Met Asp
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20 25 30

Thr Arg Thr Leu Glu Glu Val Gly Lys Val Phe Gly Val Thr Arg Glu
35 40 45

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Ser Arg Ser
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cat cgt aat aag gag cac aaa aca ata gat aat gta cca act gct aac 96
His Arg Asn Lys Glu His Lys Thr Ile Asp Asn Val Pro Thr Ala Asn
20 25 30

tta gtt gat tgg tac cct cta agt aat gct tat gag tac aag tta agt 144
Leu Val Asp Trp Tyr Pro Leu Ser Asn Ala Tyr Glu Tyr Lys Leu Ser
35 40 45

aga aac ggg gaa tac tta gaa tta aaa aga tta cgt tct act tta cct	192
Arg Asn Gly Glu Tyr Leu Glu Leu Lys Arg Leu Arg Ser Thr Leu Pro	
50 55 60	
tca tct tat ggt tta gat gat aat aac caa gat att att aga gat aat	240
Ser Ser Tyr Gly Leu Asp Asp Asn Asn Gln Asp Ile Ile Arg Asp Asn	
65 70 75 80	
aac cat aga tgt aaa ata ggt tat tgg tac aac cct gca gta cgc aaa	288
Asn His Arg Cys Lys Ile Gly Tyr Trp Tyr Asn Pro Ala Val Arg Lys	
85 90 95	
gat aat tta aag att ata gag aaa gct aaa caa tat gga tta cct att	336
Asp Asn Leu Lys Ile Ile Glu Lys Ala Lys Gln Tyr Gly Leu Pro Ile	
100 105 110	
ata aca gaa gaa tat gat gct aat act gta gag caa gga ttt aga gat	384
Ile Thr Glu Glu Tyr Asp Ala Asn Thr Val Glu Gln Gly Phe Arg Asp	
115 120 125	
att gga gtt ata ttc caa agt ctt aaa act att gtt gtt act aga tac	432
Ile Gly Val Ile Phe Gln Ser Leu Lys Thr Ile Val Val Thr Arg Tyr	
130 135 140	
cta gaa ggt aaa aca gaa gaa gaa tta aga ata ttt aac atg aaa tca	480
Leu Glu Gly Lys Thr Glu Glu Glu Leu Arg Ile Phe Asn Met Lys Ser	
145 150 155 160	
gaa gag tca caa ctg aat gaa gca ctt aaa gag agt gat ttt tct gta	528
Glu Glu Ser Gln Leu Asn Glu Ala Leu Lys Glu Ser Asp Phe Ser Val	
165 170 175	
gat tta act tat agt gac tta gga caa att tat aat atg ttg tta tta	576
Asp Leu Thr Tyr Ser Asp Leu Gly Gln Ile Tyr Asn Met Leu Leu Leu	
180 185 190	
atg aaa aaa att agt aaa tag	597
Met Lys Lys Ile Ser Lys	
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35 40 45

Arg Asn Gly Glu Tyr Leu Glu Leu Lys Arg Leu Arg Ser Thr Leu Pro
50 55 60

Ser Ser Tyr Gly Leu Asp Asp Asn Asn Gln Asp Ile Ile Arg Asp Asn
65 70 75 80

Asn His Arg Cys Lys Ile Gly Tyr Trp Tyr Asn Pro Ala Val Arg Lys
85 90 95

Asp Asn Leu Lys Ile Ile Glu Lys Ala Lys Gln Tyr Gly Leu Pro Ile
100 105 110

Ile Thr Glu Glu Tyr Asp Ala Asn Thr Val Glu Gln Gly Phe Arg Asp
115 120 125

Ile Gly Val Ile Phe Gln Ser Leu Lys Thr Ile Val Val Thr Arg Tyr
130 135 140

Leu Glu Gly Lys Thr Glu Glu Glu Leu Arg Ile Phe Asn Met Lys Ser
145 150 155 160

Glu Glu Ser Gln Leu Asn Glu Ala Leu Lys Glu Ser Asp Phe Ser Val
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 180 185 190

Met Lys Lys Ile Ser Lys
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His Arg Cys Lys Ile Gly Tyr Trp Tyr Asn Pro Ala Val Arg Lys Asp
 35 40 45

Asn Leu Lys Ile Ile Glu Lys Ala Lys Gln Tyr Gly Leu Pro Ile Ile
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Thr Glu Glu Tyr Asp Ala Asn Thr Val Glu Gln Gly Phe Arg Asp Ile
 65 70 75 80

Gly Val Ile Phe Gln Ser Leu Lys Thr Ile Val Val Thr Arg Tyr Leu
 85 90 95

Glu Gly Lys Thr Glu Glu Glu Leu Arg Ile Phe Asn Met Lys Ser Glu
 100 105 110

Glu Ser Gln Leu Asn Glu Ala Leu Lys Glu Ser Asp Phe Ser Val Asp
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Lys Lys Ile Ser Lys
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 Asn Ser Met Gly Val Thr Lys Leu Asp Val Pro Leu Ser Asn Ile His
 20 25 30
 gaa tgg tat cct ttt tct aac gct tat tct tac aag tat aat gta aaa 144
 Glu Trp Tyr Pro Phe Ser Asn Ala Tyr Ser Tyr Lys Tyr Asn Val Lys
 35 40 45
 aca aaa gat tta gta tta aaa cga cta cgt tca tca cta cca gta tct 192
 Thr Lys Asp Leu Val Leu Lys Arg Leu Arg Ser Ser Leu Pro Val Ser
 50 55 60
 tat ggg att gaa cga gcg tct aaa gag tat gac aaa gat aaa gta tgt 240
 Tyr Gly Ile Glu Arg Ala Ser Lys Glu Tyr Asp Lys Asp Lys Val Cys
 65 70 75 80
 aac aca gta aca tgg ata aac cat tca gta aaa gac agt aat tta cac 288
 Asn Thr Val Thr Trp Ile Asn His Ser Val Lys Asp Ser Asn Leu His
 85 90 95
 att att aat aaa gct aaa tca tat ggg tta cct gtt att aca gaa aag 336

Ile	Ile	Asn	Lys	Ala	Lys	Ser	Tyr	Gly	Leu	Pro	Val	Ile	Thr	Glu	Lys	
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tat	aca	tat	gaa	gat	gtg	gat	tat	ggg	ttt	gca	cag	tta	aat	gtt	atc	384
Tyr	Thr	Tyr	Glu	Asp	Val	Asp	Tyr	Gly	Phe	Ala	Gln	Leu	Asn	Val	Ile	
			115				120					125				
ttt	tct	gaa	tta	aaa	tct	ttg	att	att	aat	cgt	tat	tta	gag	gat	aaa	432
Phe	Ser	Glu	Leu	Lys	Ser	Leu	Ile	Ile	Asn	Arg	Tyr	Leu	Glu	Asp	Lys	
			130				135				140					
gat	ggt	agt	ttt	att	gtt	aag	ttt	aaa	aga	cac	aac	cca	gaa	acc	caa	480
Asp	Gly	Ser	Phe	Ile	Val	Lys	Phe	Lys	Arg	His	Asn	Pro	Glu	Thr	Gln	
					150					155					160	
tat	cat	tta	gcg	gta	caa	gat	gct	gat	gag	gtt	att	aat	aat	acc	tat	528
Tyr	His	Leu	Ala	Val	Gln	Asp	Ala	Asp	Glu	Val	Ile	Asn	Asn	Thr	Tyr	
				165					170					175		
gat	gag	cta	ggt	caa	atg	tat	aaa	atg	tta	tta	cta	atg	aag	aaa	tta	576
Asp	Glu	Leu	Gly	Gln	Met	Tyr	Lys	Met	Leu	Leu	Leu	Met	Lys	Lys	Leu	
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Ser	Lys	Tyr														
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<210> 10
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			20					25					30		
Glu	Trp	Tyr	Pro	Phe	Ser	Asn	Ala	Tyr	Ser	Tyr	Lys	Tyr	Asn	Val	Lys
			35				40					45			

Thr Lys Asp Leu Val Leu Lys Arg Leu Arg Ser Ser Leu Pro Val Ser
50 55 60

Tyr Gly Ile Glu Arg Ala Ser Lys Glu Tyr Asp Lys Asp Lys Val Cys
65 70 75 80

Asn Thr Val Thr Trp Ile Asn His Ser Val Lys Asp Ser Asn Leu His
85 90 95

Ile Ile Asn Lys Ala Lys Ser Tyr Gly Leu Pro Val Ile Thr Glu Lys
100 105 110

Tyr Thr Tyr Glu Asp Val Asp Tyr Gly Phe Ala Gln Leu Asn Val Ile
115 120 125

Phe Ser Glu Leu Lys Ser Leu Ile Ile Asn Arg Tyr Leu Glu Asp Lys
130 135 140

Asp Gly Ser Phe Ile Val Lys Phe Lys Arg His Asn Pro Glu Thr Gln
145 150 155 160

Tyr His Leu Ala Val Gln Asp Ala Asp Glu Val Ile Asn Asn Thr Tyr
165 170 175

Asp Glu Leu Gly Gln Met Tyr Lys Met Leu Leu Leu Met Lys Lys Leu
180 185 190

Ser Lys Tyr
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<211> 30
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<210> 38
 <211> 29
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 <220>
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<210> 40
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 <213> artificial sequence

 <220>
 <223> Sequence is completely synthesized

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<210> 41
<211> 49
<212> DNA
<213> artificial sequence

<220>
<223> Sequence is completely synthesized

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49